## STIC Biotechnology Systems Branch

## **RAW SEQUENCE LISTING** ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

**Application Serial Number:** 

Source:

Date Processed by STIC:

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS. PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<a href="http://www.uspto.gov/ebc/efs/downloads/documents.htm">http://www.uspto.gov/ebc/efs/downloads/documents.htm</a>, EFS Submission User Manual - ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

| ERROR DETECTED   | SUGGESTED CORRECTION SERIAL NUMBER: 10/568,737  |  |  |  |  |  |  |  |  |  |  |
|--|---|--|--|--|--|--|--|--|--|--|--|
| ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE |   |  |  |  |  |  |  |  |  |  |  |
| 1Wrapped Nucleics<br>Wrapped Aminos  | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."  |  |  |  |  |  |  |  |  |  |  |
| 2Invalid Line Length   | The rules require that a line not exceed 72 characters in length. This includes white spaces.   |  |  |  |  |  |  |  |  |  |  |
| 3Misaligned Amino<br>Numbering   | The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do <b>not</b> use tab codes between numbers; use <b>space characters</b> , instead.  |  |  |  |  |  |  |  |  |  |  |
| 4Non-ASCII   | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.  |  |  |  |  |  |  |  |  |  |  |
| 5Variable Length   | Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.  |  |  |  |  |  |  |  |  |  |  |
| 6PatentIn 2.0 "bug"  | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.  |  |  |  |  |  |  |  |  |  |  |
| 7Skipped Sequences<br>(OLD RULES)  | Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.  |  |  |  |  |  |  |  |  |  |  |
| 8Skipped Sequences (NEW RULES)   | Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number component of the sequ |  |  |  |  |  |  |  |  |  |  |
| 9Use of n's of Xaa's<br>(NEW BULES)  | Use of n's and/or Xaa's have been detected in the Sequence Listing.  Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.  |  |  |  |  |  |  |  |  |  |  |
| 10Invalid <213><br>Response  | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)  |  |  |  |  |  |  |  |  |  |  |
| 11Use of <220>   | Sequence(s)missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules   |  |  |  |  |  |  |  |  |  |  |
| PatentIn 2.0 "bug"   | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.   |  |  |  |  |  |  |  |  |  |  |
| 13 Misuse of n/Xaa   | "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid  |  |  |  |  |  |  |  |  |  |  |
|  |   |  |  |  |  |  |  |  |  |  |  |



**IFWP** 

RAW SEQUENCE LISTING DATE: 02/27/2006
PATENT APPLICATION: US/10/568,737 TIME: 15:06:53

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\02272006\J568737.raw

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3 <110> APPLICANT: SHIRE BIOCHEM INC.
     5 <120> TITLE OF INVENTION: POLYPEPTIDES OF STREPTOCOCCUS PYOGENES
     7 <130> FILE REFERENCE: 51564-44
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/568,737
C--> 10 <141> CURRENT FILING DATE: 2006-02-15
     12 <150> PRIOR APPLICATION NUMBER: US 60/495,094
                                                               Dres Met Cemply
     13 <151> PRIOR FILING DATE: 2003-08-15
                                                               Corrected Distroits Neoded)
     15 <160> NUMBER OF SEQ ID NOS: 44
     17 <170> SOFTWARE: PatentIn version 3.3
     19 <210> SEQ ID NO: 1
     20 <211> LENGTH: 537
     21 <212> TYPE: DNA
    22 <213> ORGANISM: Streptococcus pyogenes
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    27 aacaatgtta ttactgttaa aggccctaaa ggcgaactca ctcgtgagtt caacaaaaat
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    29 attgaaatca aagttgaagg gactgaaatc acagttgtac gtcctaacga ctcaaaagaa
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     31 atgaaaacaa tecatggtac aaccegtget aacttgaata acatggttgt aggtgtttet
                                                                              240
     33 gaaggtttca aaaaagatct tgaaatgaag ggtgtcggtt accgtgctca acttcaaggt
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     35 actaaacttg tcctttcagt aggtaaatct caccaagacg aagttgaagc tccagaagga
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    37 attactttca ctgttgctaa cccaacttca atctcagttg aaggaatcaa caaagaagtt
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    39 gttggtcaaa cagctgctta catccgtagc ttgcgttcac cagagcctta caaaggcaaa
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    41 gggatccgtt acgttggtga atacgtacgc cttaaagaag gtaaaacagg taaataa
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                                            10
    55 Leu Thr Asn Asn Asn Asn Val Ile Thr Val Lys Gly Pro Lys Gly Glu
                    20
                                        25
                                                            30
     59 Leu Thr Arg Glu Phe Asn Lys Asn Ile Glu Ile Lys Val Glu Gly Thr
               35
                                    40
     63 Glu Ile Thr Val Val Arg Pro Asn Asp Ser Lys Glu Met Lys Thr Ile
     67 His Gly Thr Thr Arg Ala Asn Leu Asn Asn Met Val Val Gly Val Ser
                                                75
                            70
     71 Glu Gly Phe Lys Lys Asp Leu Glu Met Lys Gly Val Gly Tyr Arg Ala
                        85
                                            90
    75 Gln Leu Gln Gly Thr Lys Leu Val Leu Ser Val Gly Lys Ser His Gln
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79 Asp Glu Val Glu Ala Pro Glu Gly Ile Thr Phe Thr Val Ala Asn Pro

RAW SEQUENCE LISTING DATE: 02/27/2006
PATENT APPLICATION: US/10/568,737 TIME: 15:06:53

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Output Set: N:\CRF4\02272006\J568737.raw

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83 Thr Ser Ile Ser Val Glu Gly Ile Asn Lys Glu Val Val Gly Gln Thr
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87 Ala Ala Tyr Ile Arg Ser Leu Arg Ser Pro Glu Pro Tyr Lys Gly Lys
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91 Gly Ile Arg Tyr Val Gly Glu Tyr Val Arg Leu Lys Glu Gly Lys Thr
92
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                                       170
95 Gly Lys
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102 <213> ORGANISM: Streptococcus pyogenes
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107 ttgacctgtg tggttggtgg tagctacttg ataatgaacc atcaacaaca agaaattgtc
                                                                          120
109 tctagtgtca acaaagtaaa agccttaacc ataaaagaag ccatggaaca aggaaaagat
                                                                          180
111 atcagcttga ccttagctgg cgaagtaaca gctaacaaca gcagcaaagt caaaatcgac
                                                                          240
113 tcaagtaaag gagaagtcaa agaggtcttt gttaaaaaag gcgatgttgt caaagtagga
                                                                          300
115 caaccettgt ttagetatga aacgtcacag cggttaacgg ctcaaagttc agaatttgat
                                                                          360
117 gttcaaacca aagccaatca gctccaagtt gctaaaacca atgcagcatt gaagtgggaa
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119 acctacaatc gcaaggtcaa tgaaatcaac accctaaaat ctcgctacaa cactgcacca
                                                                          480
121 gatgagaget tactagagea aattegeage geagaagaea gtgtateeea ageactaage
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123 gatgccaaaa cagcagatag cgatgtcaaa accgctcaaa tcgaactcga taaagctaat
                                                                          600
125 gctactgcca caacggaaaa aggtaaacta gagtatgaca ccgttaagtc agacaccgca
                                                                          660
                                                                          720
127 ggaaccattq ttaqtctaaa tactqatttq ccaaatcaat caaaatccaa aaaagaaaat
129 gaaactttta tqqaaattat cqacaaatca aaaatqttaq tcaaaqqtaa cattaqtgaa
                                                                          780
131 tttgaccgtg acaagttaaa aatcggtcaa aaagtcgaag tgattgaccg caaagacaac
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133 tctaaaaaat ggactggaaa agtaacccaa gttggcaacc tcaaagcaga ggaaaaaggc
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135 caaggtcaag gccaaggtgg caatgaccaa caagataatc caaaccaagc aaaattccct
                                                                          960
137 tatgttattg aacttgacca atcagacaag cagccactca ttggctcaca cacctatgtt
                                                                         1020
139 aatgtgctca acaatgttcc agaagctggc aagatcgtat tgaaagaaac ctttacaatg
                                                                         1080
141 gcagaaaatg gaaaaaccta tgtgtggaaa gttgataaaa acaaggtcaa aaaacaagaa
                                                                         1140
143 atcaaqacta agcccttctc aaaaqqttat qttqaqqtaa caaqtqqctt qactatqcaa
                                                                         1200
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150 <210> SEQ ID NO: 4
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152 <212> TYPE: PRT
153 <213> ORGANISM: Streptococcus pyogenes
155 <400> SEQUENCE: 4
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162
165 Asn His Gln Gln Gln Glu Ile Val Ser Ser Val Asn Lys Val Lys Ala
                                40
169 Leu Thr Ile Lys Glu Ala Met Glu Gln Gly Lys Asp Ile Ser Leu Thr
                            55
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173 Leu Ala Gly Glu Val Thr Ala Asn Asn Ser Ser Lys Val Lys Ile Asp

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PATENT APPLICATION: US/10/568,737 TIME: 15:06:53

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Output Set: N:\CRF4\02272006\J568737.raw

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174 65
177 Ser Ser Lys Gly Glu Val Lys Glu Val Phe Val Lys Lys Gly Asp Val
                    85
                                        90
181 Val Lys Val Gly Gln Pro Leu Phe Ser Tyr Glu Thr Ser Gln Arg Leu
                                   105
185 Thr Ala Gln Ser Ser Glu Phe Asp Val Gln Thr Lys Ala Asn Gln Leu
        115
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189 Gln Val Ala Lys Thr Asn Ala Ala Leu Lys Trp Glu Thr Tyr Asn Arq
      130
                           135
193 Lys Val Asn Glu Ile Asn Thr Leu Lys Ser Arg Tyr Asn Thr Ala Pro
                       150
197 Asp Glu Ser Leu Leu Glu Gln Ile Arg Ser Ala Glu Asp Ser Val Ser
                   165
                                        170
201 Gln Ala Leu Ser Asp Ala Lys Thr Ala Asp Ser Asp Val Lys Thr Ala
                                    185
205 Gln Ile Glu Leu Asp Lys Ala Asn Ala Thr Ala Thr Thr Glu Lys Gly
           195
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209 Lys Leu Glu Tyr Asp Thr Val Lys Ser Asp Thr Ala Gly Thr Ile Val
                           215
213 Ser Leu Asn Thr Asp Leu Pro Asn Gln Ser Lys Ser Lys Glu Asn
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                                            235
217 Glu Thr Phe Met Glu Ile Ile Asp Lys Ser Lys Met Leu Val Lys Gly
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221 Asn Ile Ser Glu Phe Asp Arg Asp Lys Leu Lys Ile Gly Gln Lys Val
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                                    265
225 Glu Val Ile Asp Arg Lys Asp Asn Ser Lys Lys Trp Thr Gly Lys Val
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229 Thr Gln Val Gly Asn Leu Lys Ala Glu Glu Lys Gly Gln Gly Gln Gly
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233 Gln Gly Gly Asn Asp Gln Gln Asp Asn Pro Asn Gln Ala Lys Phe Pro
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                                            315
237 Tyr Val Ile Glu Leu Asp Gln Ser Asp Lys Gln Pro Leu Ile Gly Ser
                    325
                                       330
241 His Thr Tyr Val Asn Val Leu Asn Asn Val Pro Glu Ala Gly Lys Ile
               340
                                    345
245 Val Leu Lys Glu Thr Phe Thr Met Ala Glu Asn Gly Lys Thr Tyr Val
    355
                               360
249 Trp Lys Val Asp Lys Asn Lys Val Lys Lys Gln Glu Ile Lys Thr Lys
                            375
       370
                                                380
253 Pro Phe Ser Lys Gly Tyr Val Glu Val Thr Ser Gly Leu Thr Met Gln
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257 Asp Lys Ile Ala Gln Pro Leu Pro Gly Met Lys Asp Gly Met Glu Val
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266 <211> LENGTH: 885
267 <212> TYPE: DNA
268 <213> ORGANISM: Streptococcus pyogenes
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PATENT APPLICATION: US/10/568,737 TIME: 15:06:53

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\02272006\J568737.raw

| 271 atgataaaac gatgtaaaag aattggtcta gccttaatgg ccttctttt ggtagcttg   | 270 | <400                                    | > SE           | OUEN | ICE :     | 5      |       |           |       |        |         |         |      |        |        |       |        |  |     |
|---|-----|---|----------------|------|-----------|--------|-------|-----------|-------|--------|---------|---------|------|--------|--------|-------|--------|--|-----|
| 273 gtgaatcagc accctaaaac ggctaaagag actgaacagc agagaattgt agccattcg 275 gttgctgtgg ttgatactg tgaccgttta aatttagacc tcgttggggt ttgtgatagt 276 aatttataa cccttcctaa acgctatgat gctgtaagc gtgtgggtt acccatgaa 277 aaattatata cccttcctaa acgctatgat gctgtaagc gtgtgggtt acccatgaa 278 cctgatatag agttgattgc ttcttttgaaa ccaacttgga tttttgagtc caattctta 280 caagaagatt tgaacccaa gatatcaaaaa ttggatactt gatatgtt tttgaactta 281 caagaagatt agagcatga ccagcacatc gatgatttag ggaaccttt ccaacctaaa 282 caagaaggad agaaaaagcc caagcacatc attctatag gctagccaag tagttatttg 283 cgaagtgttg agggaatgc caagcacatc attctatag gctagccaag tagttatttg 284 gtggcgacga acaaactta tgtagggat attctatagg gctgccaag tagttatttg 285 gtggcgacga accaatctta tgtagggat cttttggact tggcaggtg tgagaatgt 286 caagaagttg ctgaagaaaga atttctacag cagtaacacca aggtaaaagt gatgttagc 287 ctgaaggga agaaaaaga tattttagaa catttcaga cagcacagaagagagaagc 293 cctgacttga ttttacgaac agctcatgc attccagaca aggtaaaagt gatgttga 295 aaagaatttg ctgaaaataga tatttgagaa cattttacag cagtcaagaag agggaaagt 296 gacaccttaa cacagctttt tgaccacgtg ggagatcatc cgtaa 297 tatgatttgg acaaataccc gtttggcatg agtgctaaat tgaactaccc agaagccttg 298 gacaccttaa cacagctttt tgaccacgtg ggagatcatc 299 gacaccttaa cacagctttt tgaccacgtg ggagatcatc 290 cylo> SEQ ID NO: 6 291 cylo> SEQ ID NO: 6 292 cylo> SEQ ID NO: 6 293 cylo> SEQ ID NO: 6 294 cylo> SEQ ID NO: 6 295 cylo> SEQ ID NO: 6 296 cylo> SEQ ID NO: 6 297 tatgattga cacagagagacaccagagagacaccaccagagagacaccac  |     |   |                | _    |           |        | aq aa | attac     | atcta | a acc  | cttaa   | ataa    | cctt | cttt   | tt d   | artac | acttat |  | 60  |
| 275 qttgctgttgg ttgatatctg tgaccgttta aatttagacc tcgttgggtt tdgtgatagt  |     |   |                |      |           |        |       |           |       |        |         |         |      |        |        |       |        |  | 120 |
| 277 aaattatata cccttcctaa acgctatgat gctgttaagc gtgtgggtt accctgaat   |     |   |                |      |           |        |       |           |       |        |         |         |      |        |        |       |        |  |     |
| 279 ctgatatag agttgattgc ttctttgaaa ccaacttgga ttttgagtcc caattcttta 360 281 caagaagatt tggaaccaa gatcaaaaa ttggatactg agtatggtt tttgaactta 360 283 cgaagagaa aggagtgtg accagtcatt gatgatttag ggaaccttt ccaacgtcaa 420 285 caagaagcaa aagaattgcg ccagcaatac caggactatt atcgtgcttt ccaacgtcaa 480 287 cgtaagggga agcaaatctta tgtagggaat cttttagg gcttgccagg tagtatttg 540 289 gtggcgacga accaatctta tgtagggaat cttttagg cttgccagg tagtatttg 540 299 gtacacttga ttttacgaac agctaatccd agacacaaca aggtaaaagg 660 291 cttcagtcag atgagaaaaga atttctatca gctaatcctg aagacatgct ggctaaagag 393 cctgacttga ttttacgaac agtcatagcc attccaagaca aggtaaaagg aggtaaagac 720 295 aaagaattg ctgaaaatga tatttggaac catttacgg cagtcaaaga aggtaaaagt 720 295 aaagaattg ctgaaaatga tatttggaac catttacgg cagtcaaaga agggaaagtc 720 295 aaagaattg ctgaaaatga tattggaac catttacgg cagtcaaaga agggaaagtc 720 297 gacaccttaa ccacgctttt tgaccacgtg ggagatcac cgtaa 230 297 tatgatttgg accaatacct gtttggcatg aggaatcac cgtaa 230 297 ctagatttg ctgaaaatga tattggaac catttacgg cagtcaaaga agggaaagtc 720 298 gacaccttaa cacagctttt ttgaccacgtg ggagatcac cgtaa 230 299 gacaccttaa cacagctttt tgaccacgtg ggagatcac cgtaa 230 201  |     |   |                |      |           |        |       |           |       |        |         |         |      |        |        |       |        |  |     |
| 281 caagaagatt tggaacccaa gtatcaaaaa ttggatattg agtatgttt tttgaactta  |     |   |                |      |           |        |       |           |       |        |         |         |      |        |        |       |        |  |     |
| 283 cgaagtgttg agggcatgta ccagtccatt gatgatttag ggaacetttt ccaacgtcaa 420 285 caagaagcaa aagaattgcg ccagcaatac caggactatt atcgtgettt ccaagctaaa 480 287 cgtaagggga agaaaaagcc taaagtgctt attettatgg gettgccagg tagttatttg 540 289 gtggcgacga accaatctta tgtagggaat ctttttggact tggcaaggtg tgagaatgtt 600 291 tatcagtcag atgagaaaaga atttctatca getaatectg aagactaget ggetaaggag 660 293 cctgacttga ttttacgaac agctcatgcc attccagaca aggtaaaagt ggetaaggag 720 295 aaagaatttg ctgaaaatga tattttggaaa cattttacgg cagtcaagga agggaaagtc 720 295 aaagaatttg ctgaaaatga tatttggaaa cattttacgg cagtcaagga agggaaagtc 720 295 aaagaatttg ctgaaaatga tatttggaaa cattttacgg cagtcaagga agggaaagtc 720 296 gacaccttaa cacagctttt tgaccacgtg ggagatcatc cgtaa 192 297 tatgatttgg acaataccct gtttggcatg agtgctaaat tgaactaccc agaagcttg 880 298 c210  |     |   |                |      |           |        |       |           |       |        |         |         |      |        |        |       |        |  |     |
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| 287 cgtaagggga agaaaaagcc taaagtgctt attcttatgg gcttgccagg tagtatttg  |     | * * = = *** = = = = = = = = = = = = = = |                |      |           |        |       |           |       |        |         |         |      |        |        |       |        |  |     |
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| 309 Met   11e   1ys   Arg   Cys   Lys   Gly   11e   Gly   Leu   Ala   Leu   Met   Ala   Phe   Phe   310   1   |     |   |                |      |           |        | -pco. |           | , P   | , 0901 | 100     |         |      |        |        |       |        |  |     |
| 310   1   |     |   |                |      |           |        | Lvc   | Glv       | Tle   | Glv    | T.e.11  | Δla     | Len  | Met    | Δla    | Phe   | Phe    |  |     |
| 313 Leu Val Ala Cys Val Asn Gln His Pro Lys Thr Ala Lys Glu Thr Glu 314   |     |   | 110.           | цуз  | nr 9      |        | цуз   | Oly       | 110   | Ory    |         | 1114    | БСС  | 1100   | 1114   |       | 1110   |  |     |
| 314   |     |   | (/a)           | Δla  | Cvc       | _      | Δen   | Gln       | Hic   | Pro    |         | Thr     | Δla  | Lvc    | Glu    |       | Glu    |  |     |
| 317 Gln Gln Arg Ile Val Ala Thr Ser Val Ala Val Val Asp Ile Cys Asp 318   |     | пец                                     | vai            | AIG  | -         | val    | HOII  | 0111      | 1113  |        | цур     | 1111    | niu  | Lys    |        | 1111  | Olu    |  |     |
| 318   |     | Gln (                                   | Gl n           | λνα  |           | Wa 1   | Δla   | Thr       | Sor   |        | בומ     | Val     | Val  | Acn    |        | Cve   | Δen    |  |     |
| 321       Arg       Leu       Asn       Leu       Val       Gly       Val       Cys       Asp       Ser       Lys       Leu       Tyr       Thr         322       50       50       55       60       60       325       Leu       Pro       Lys       Arg       Tyr       Asp       Ala       Val       Lys       Arg       Val       Gly       Leu       Pro       Met       Asn         326       65       65       70       70       75       75       80         329       Pro       Asp       Ile       Glu       Leu       Ile       Ala       Ser       Leu       Lys       Pro       Thr       Trp       Ile       Leu       Ser         333       Pro       Asn       Ser       Leu       Glu       Asp       Leu       Glu       Lys       Tyr       Ile       Leu       Asp         341       Tr       Glu       Tr       Gly       Phe       Leu       Arg       Ser       Val       Glu       Glu       Glu       Ala       Lys       Lys       Ile       Ala       Lys       Ile       Ile       Ile       Ile       Ile       Ile   |     | GIII                                    | G111           | _    | 110       | Vai    | ALU   | 1111      |       | vai    | niu     | vai     | vai  | _      | 110    | Cyb   | 715P   |  |     |
| 322       50       55       60         325       Leu Pro Lys Arg Tyr Asp Ala Val Lys Arg Val Gly Leu Pro Met Asn         326       65       70       70       75       80         329       Pro Asp Ile Glu Leu Ile Ala Ser Leu Lys Pro Thr Trp Ile Leu Ser       80         330       85       90       95         331       Pro Asn Ser Leu Gln Glu Asp Leu Glu Pro Lys Tyr Gln Lys Leu Asp       110         337       Thr Glu Tyr Gly Phe Leu Asn Leu Arg Ser Val Glu Gly Met Tyr Gln       110         338       115       120       125         341       Ser Ile Asp Asp Leu Gly Asn Leu Phe Gln Arg Gln Gln Glu Ala Lys         342       130       135       140         345       Glu Leu Arg Gln Gln Tyr Gln Asp Tyr Tyr Arg Ala Phe Gln Ala Lys         346       145       150       155       160         349       Arg Lys Gly Lys Lys Lys Lys Pro Lys Val Leu Ile Leu Met Gly Leu Pro         350       165       170       175         353       Gly Ser Tyr Leu Val Ala Thr Asn Gln Ser Tyr Val Gly Asn Leu Leu         354       180       185       190         355       180       185       190         356       195       200       205         361       Leu   |     | Ara .                                   | T. <b>-</b> 11 |      | T.011     | Aen    | T.011 | Val       |       | Val    | Cve     | Δsn     | Ser  |        | T.e.11 | Tur   | Thr    |  |     |
| 325         Leu         Pro         Lys         Arg         Tyr         Asp         Ala         Val         Lys         Arg         Leu         Pro         Ass           326         65         -         -         70         -         -         75         -         -         80           329         Pro         Asp         Ile         Glu         Leu         Ile         Ala         Ser         Leu         Lys         Pro         Thr         Trp         Ile         Leu         Ser           330         Pro         Asn         Ser         Leu         Glu         Asp         Leu         Asp         Leu         Glu         Fro         Lys         Tyr         Glu         Lys         Leu         Asp           334         -         100         -         -         -         105         -         -         -         110         -   |     | _                                       |                | LOII | ncu       | пор    | пси   |           | OLY   | vui    | Cys     | лор     |      | БуБ    | пси    | - 7 - |        |  |     |
| 326       65       70       75       80         329       Pro Asp Ile Glu Leu Ile Glu Leu Ile Ala Ser Leu Lys Pro Thr Trp Ile Leu Ser         330       85       90       95         333       Pro Asn Ser Leu Gln Glu Asp Leu Glu Pro Lys Tyr Gln Lys Leu Asp         334       100       105       110         337       Thr Glu Tyr Gly Phe Leu Asn Leu Arg Ser Val Glu Gly Met Tyr Gln       110         338       115       120       125         341       Ser Ile Asp Asp Leu Gly Asn Leu Phe Gln Arg Gln Gln Gln Glu Ala Lys         342       130       135       140         345       Glu Leu Arg Gln Gln Tyr Gln Asp Tyr Tyr Arg Ala Phe Gln Ala Lys       160         349       Arg Lys Gly Lys Lys Lys Pro Lys Val Leu Ile Leu Met Gly Leu Pro         350       165       170         353       Gly Ser Tyr Leu Val Ala Thr Asn Gln Ser Tyr Val Gly Asn Leu Leu         354       180       185         357       Asp Leu Ala Gly Gly Glu Asn Val Tyr Gln Ser Asp Glu Lys Glu Phe         358       195         357       Asp Leu Ala Asn Pro Glu Asp Met Leu Ala Lys Glu Pro Asp Leu Ile  |     |   |                | Lare | Δra       | ጥኒ/ዮ   | Aen   |           | Val   | Larg   | Δra     | Val     |      | I.e.ii | Pro    | Met   | Δan    |  |     |
| 329       Pro Asp Ile Glu Leu Ile Ala Ser Leu Lys Pro Thr Trp Ile Leu Ser         330       85       90       95         333       Pro Asn Ser Leu Gln Glu Asp Leu Glu Pro Lys Tyr Gln Lys Leu Asp         334       100       105       110         337       Thr Glu Tyr Gly Phe Leu Asn Leu Arg Ser Val Glu Gly Met Tyr Gln       125         341       Ser Ile Asp Asp Leu Gly Asn Leu Phe Gln Arg Gln Gln Gln Glu Ala Lys         342       130       135         345       Glu Leu Arg Gln Gln Tyr Gln Asp Tyr Tyr Arg Ala Phe Gln Ala Lys         346       145       150         349       Arg Lys Gly Lys Lys Lys Pro Lys Val Leu Ile Leu Met Gly Leu Pro         350       165         353       Gly Ser Tyr Leu Val Ala Thr Asn Gln Ser Tyr Val Gly Asn Leu Leu         354       180         357       Asp Leu Ala Gly Gly Glu Asn Val Tyr Gln Ser Asp Glu Lys Glu Phe         358       195         357       Asp Leu Ala Gly Gly Glu Asn Val Tyr Gln Ser Asp Glu Lys Glu Phe         358       195         351       190         352       195  |     |   | 110            | цуз  | nrg       | 1 7 1  |       | AIG       | vai   | цуз    | nr 9    |         | Ory  | ыси    | 110    | rice  |        |  |     |
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| 333 Pro Asn Ser Leu Gln Glu Asp Leu Glu Pro Lys Tyr Gln Lys Leu Asp 334   |     | 110                                     | op             | 110  | OI u      |        |       | 1114      | 501   | Leu    | _       |         |      | 115    |        |       | 502    |  |     |
| 334       100       105       110         337       Thr Glu Tyr Gly Phe Leu Asn Leu Arg Ser Val Glu Gly Met Tyr Gln         338       115       120       125         341       Ser Ile Asp Asp Leu Gly Asn Leu Phe Gln Arg Gln Gln Glu Ala Lys         342       130       135       140         345       Glu Leu Arg Gln Gln Tyr Gln Asp Tyr Tyr Arg Ala Phe Gln Ala Lys         346       145       150       150         349       Arg Lys Gly Lys Lys Lys Pro Lys Val Leu Ile Leu Met Gly Leu Pro         350       165       170       175         353       Gly Ser Tyr Leu Val Ala Thr Asn Gln Ser Tyr Val Gly Asn Leu Leu         354       180       185       190         357       Asp Leu Ala Gly Gly Glu Asn Val Tyr Gln Ser Asp Glu Lys Glu Phe         358       195       200         361       Leu Ser Ala Asn Pro Glu Asp Met Leu Ala Lys Glu Pro Asp Leu Ile   |     | Pro                                     | Asn            | Ser  | Len       |        | Glu   | Asp       | Len   | Glu    |         | Lvs     | Tvr  | Gln    | Lvs    |       | Asp    |  |     |
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| 342       130       135       140         345       Glu Leu Arg Gln Gln Tyr Gln Asp Tyr Tyr Arg Ala Phe Gln Ala Lys         346       145       150       155       160         349       Arg Lys Gly Lys Lys Lys Lys Pro Lys Val Leu Ile Leu Met Gly Leu Pro       175       175         350       165       170       175       175         353       Gly Ser Tyr Leu Val Ala Thr Asn Gln Ser Tyr Val Gly Asn Leu Leu       190         354       180       185       190       190         357       Asp Leu Ala Gly Gly Glu Asn Val Tyr Gln Ser Asp Glu Lys Glu Phe       205         361       Leu Ser Ala Asn Pro Glu Asp Met Leu Ala Lys Glu Pro Asp Leu Ile   |     | Ser                                     | Tle            |      | Asp       | Len    | Glv   | Asn       |       | Phe    | Gln     | Ara     | Gln  |        | Glu    | Ala   | Lvs    |  |     |
| 345 Glu Leu Arg Gln Gln Tyr Gln Asp Tyr Tyr Arg Ala Phe Gln Ala Lys 346 145   |     |   |                | 1100 | 1100      | Deu    | O-1   |           | Lea   |        | 0111    | **** 9  |      | 0      | O_u    |       | 270    |  |     |
| 346       145       150       155       160         349       Arg Lys Clys Clys Lys Lys Lys Pro Lys Val Leu Ile Leu Met Cly Leu Pro         350       165       170       175         353       Gly Ser Tyr Leu Val Ala Thr Asn Gln Ser Tyr Val Gly Asn Leu Leu         354       180       185       190         357       Asp Leu Ala Gly Gly Glu Asn Val Tyr Gln Ser Asp Glu Lys Glu Phe         358       195       200         361       Leu Ser Ala Asn Pro Glu Asp Met Leu Ala Lys Glu Pro Asp Leu Ile   |     |   |                | Δrα  | Gln       | Gln    | Tvr   |           | Asn   | Tyr    | Tur     | Ara     |      | Phe    | Gln    | Δla   | Lvs    |  |     |
| 349       Arg       Lys       Gly       Lys       Lys       Lys       Val       Leu       Ile       Leu       Met       Gly       Leu       Pro         350       165       170       175       175         353       Gly       Ser       Tyr       Leu       Ile         357       Asp       Leu       Ala       Asp       Glu       Asp       Met       Leu       Ala       Leu       Asp       Leu       Ile         358       195       200       205       205       205       206       206       207       2   |     |   | ЦСЦ            | 9    | 02.11     | Q.1.1. |       | 0111      | 1100  | - 7 -  | - 7 -   |         | 1114 | 1110   | 0111   | 1114  |        |  |     |
| 350 165 170 175  353 Gly Ser Tyr Leu Val Ala Thr Asn Gln Ser Tyr Val Gly Asn Leu Leu  354 180 185 190  357 Asp Leu Ala Gly Gly Glu Asn Val Tyr Gln Ser Asp Glu Lys Glu Phe  358 195 200 205  361 Leu Ser Ala Asn Pro Glu Asp Met Leu Ala Lys Glu Pro Asp Leu Ile  |     |   | Lvs            | Glv  | Lvs       | Lvs    |       | Pro       | Lvs   | Val    | Len     |         | Len  | Met    | Glv    | Len   |        |  |     |
| 353 Gly Ser Tyr Leu Val Ala Thr Asn Gln Ser Tyr Val Gly Asn Leu Leu 354   |     | *****                                   | _, 0           | - Y  | _, 5      | -      | ~y3   |           | -y5   |        |         |         | cu   |        |        |       |        |  |     |
| 180 185 190  357 Asp Leu Ala Gly Gly Glu Asn Val Tyr Gln Ser Asp Glu Lys Glu Phe  358 195 200 205  361 Leu Ser Ala Asn Pro Glu Asp Met Leu Ala Lys Glu Pro Asp Leu Ile  |     | Glv                                     | Ser            | Tvr  | Len       |        | Δla   | Thr       | Asn   | Gln    |         | Tvr     | Val  | Glv    | Asn    |       | Leu    |  |     |
| 357 Asp Leu Ala Gly Gly Glu Asn Val Tyr Gln Ser Asp Glu Lys Glu Phe<br>358 195 200 205<br>361 Leu Ser Ala Asn Pro Glu Asp Met Leu Ala Lys Glu Pro Asp Leu Ile   |     | CTY .                                   |                | -1-  |           |        | 111 U | ****      |       |        |         | -1-     | •41  | O + Y  |        |       |        |  |     |
| 358 195 200 205<br>361 Leu Ser Ala Asn Pro Glu Asp Met Leu Ala Lys Glu Pro Asp Leu Ile  |     | Asn '                                   | T.em           | Δla  |           | Glv    | Glu   | Asn       | Val   |        | Gln     | Ser     | Asn  | Glu    |        | Glu   | Phe    |  |     |
| 361 Leu Ser Ala Asn Pro Glu Asp Met Leu Ala Lys Glu Pro Asp Leu Ile   |     |   |                |      | O-1       |        | u     | -111      |       | -1-    | <b></b> | 501     | 1105 |        | -,5    |       |        |  |     |
| •   |     | Len                                     | Ser            |      | Asn       | Pro    | Glu   | Asn       |       | Len    | Αla     | Lve     | Glu  |        | Asp    | Leu   | Ile    |  |     |
|   | 362 |   | 210            |      |           |        |       | 215       |       |        |         | _, _    | 220  |        | P      |       |        |  |     |

DATE: 02/27/2006

TIME: 15:06:53

```
Input Set : A:\PTO.RJ.txt
                Output Set: N:\CRF4\02272006\J568737.raw
365 Leu Arg Thr Ala His Ala Ile Pro Asp Lys Val Lys Val Met Phe Asp
366 225
                        230
                                            235
369 Lys Glu Phe Ala Glu Asn Asp Ile Trp Lys His Phe Thr Ala Val Lys
                    245
373 Glu Gly Lys Val Tyr Asp Leu Asp Asn Thr Leu Phe Gly Met Ser Ala
                260
                                    265
377 Lys Leu Asn Tyr Pro Glu Ala Leu Asp Thr Leu Thr Gln Leu Phe Asp
            275
                                280
381 His Val Gly Asp His Pro
                             - Invalid hospunse
        290
382
385 <210> SEQ ID NO: 7
386 <211> LENGTH: 34
387 <212> TYPE: DNA
388 <213> ORGANISM: / Primer
390 <400> SEQUENCE: \
                              Invalid Response
391 gagaaaatac atatgtcacg tattggtaat aaag
394 <210> SEQ ID NO: 8
395 <211> LENGTH: 29
396 <212> TYPE: DNA/
397 <213> ORGANISM: Primer
399 <400> SEQUENCE:
400 ccctcgagtt atttacctgt tttaccttc
403 <210> SEQ ID NO: 9
404 <211> LENGTH: 31
406 <213 > ORGANISM: Primer S AVE EVOV
                                                               erv310n
Summany
Sheeti
408 <400> SEQUENCE: >
409 aaggatccca tgtcacgtat tggtaataaa g
412 <210> SEQ ID NO: 10
413 <211> LENGTH: 38
414 <212> TYPE: DNA/
415 <213 > ORGANISM: Primer
417 <400> SEQUENCE: 10
418 actagtcgac ttatttacct gttttacctt ctttaagg
421 <210> SEQ ID NO: 11
422 <211> LENGTH: 35
                             Same erro
423 <212> TYPE: DNA
424 <213> ORGANISM: (Primer
426 <400> SEQUENCE: 31
                                                                           35
427 ccttacaaag gcaaaggcat ccgttacgtt ggtga
430 <210> SEQ ID NO: 12
431 <211> LENGTH: 35
                             Same er
432 <212> TYPE: DNA/
433 <213> ORGANISM:\Primer
435 <400> SEQUENCE: 12
436 tcaccaacgt aacggatgcc tttgcctttg taagg
                                                                           35
439 <210> SEO ID NO: 13
440 <211> LENGTH: 30
441 <212> TYPE: DNA
                                The type of errors shown exist throughout
                                the Sequence Listing. Please check subsequent
                                oppositions for similar errors.
```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/568,737

VERIFICATION SUMMARY

DATE: 02/27/2006

PATENT APPLICATION: US/10/568,737

TIME: 15:06:54

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\02272006\J568737.raw

 $\hbox{L:9 M:270 C: Current Application Number differs, Replaced Current Application}$ 

Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date